

hydrophobic, transmembrane aa1163 "Nogoes" Strep-tag Strep-tag Hise-tag aa975 ပ္ပ extracellular globular domain (Nogo-A specific) Nogo-A [aa233-aa940] Nogo-A [aa174-aa940] Nogo-A [aa233-aa940] O ပ ပ ပ proteolytic "hot spot" Strep-tag OmpA aa172 (disordered) P/A-rich E/D-rich aaī Soluble rec. fragment NI-Fr2 Soluble rec. fragment NI-Fr4 Soluble rec. fragment NI-Fr1 Nogo-A (NI-220) cDNA: Protein characteristics:

Fig. 1A

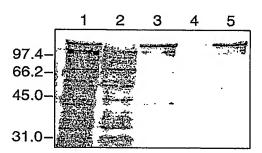


Fig. 1B

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IN-1 A32F	CDR-L1 1 24 34 40 DIELTQSPAIMAASVGETVTITC <u>GASENIYGALN</u> WYQRKQ
	CDR-L2 41 50 56 80 GKSPQLLIYGATNLADGMSSRFSGSGSGRQYSLKISSLHP
I.2.6 I.2.6(^{L96} V) II.1.8	CDR-L3 81 89 97 107 DDVATYYC <u>ONVLSTPRT</u> FGAGTKLEIK RV C RV V INRV V

Fig. 2A

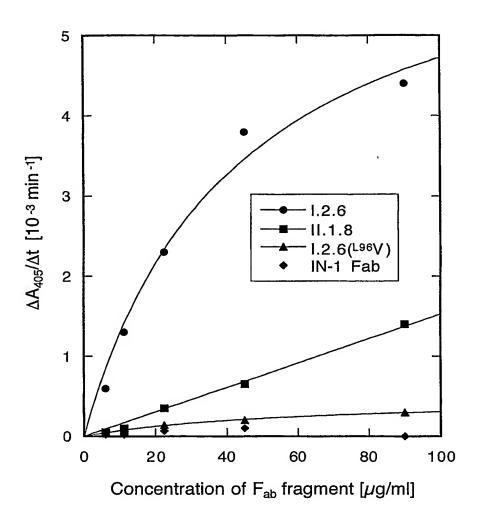


Fig. 2B

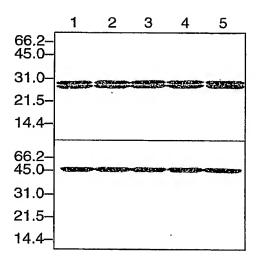


Fig. 3A

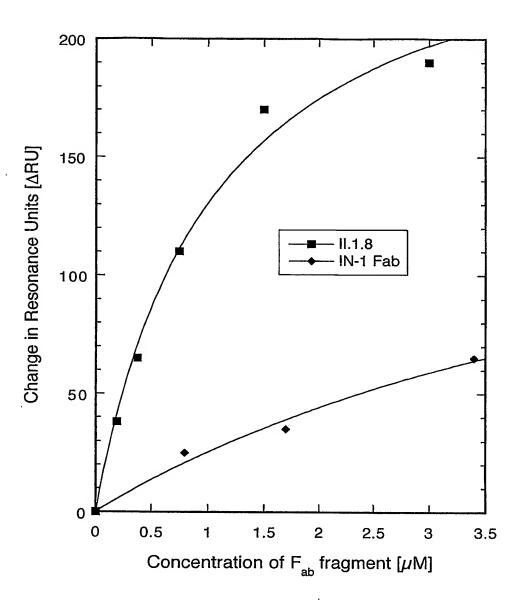


Fig. 3B

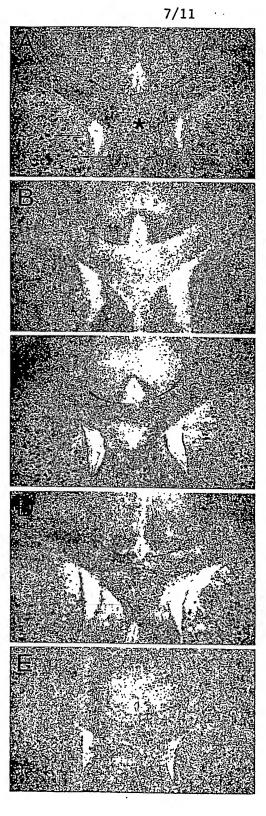


Fig. 4

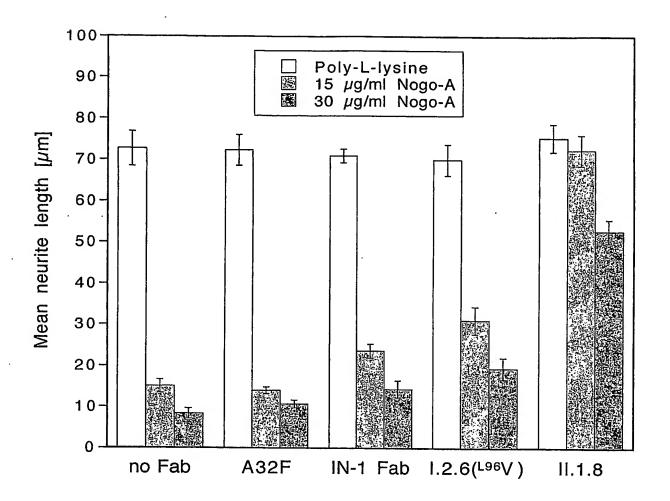
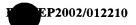


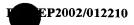
Fig. 5



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MEDIDQSSLV		~	EPEDEEDEEE	EEDEEEDDED	
LEELEVLERK	PAAGLSAAAV	PPAAAAPLLD	FSSDSVPPAP	RGPLPAAPPA	100
APERQPSWER	SPAAPAPSLP	PAAAVLPSKL	PEDDEPPARP	PPPPPAGASP	
LAEPAAPPST	PAAPKRRGSG	SVDETLFALP	AASEPVIPSS	AEKIMDLMEO	200
PGNTVSSGQE	DFPSVLLETA	ASLPSLSPLS	TVSFKEHGYL	GNLSAVSSSE	
GTIEETLNEA	SKELPERATN	PFVNRDLAEF	SELEYSEMGS	SFKGSPKGES	300
AILVENTKEE	VIVRSKDKED	LVCSAALHSP	QESPVGKEDR	VVSPEKTMDI	
FNEMQMSVVA	PVREEYADFK	PFEQAWEVKD	TYEGSRDVLA	ARANVESKVD	400
RKCLEDSLEQ	KSLGKDSEGR	NEDASFPSTP	EPVKDSSRAY	ITCASFTSAT	
ESTTANTFPL	LEDHTSENKT	DEKKIEERKA	QIITEKTSPK	TSNPFLVAVO	500
DSEADYVTTD	TLSKVTEAAV	SNMPEGLTPD	LVQEACESEL	NEATGTKIAY	
ETKVDLVQTS	EAIQESLYPT	AQLCPSFEEA	EATPSPVLPD	IVMEAPLNSL	600
LPSAGASVVQ	PSVSPLEAPP	PVSYDSIKLE	PENPPPYEEA	MNVALKALGT	
KEGIKEPESF	NAAVQETEAP	YISIACDLIK	ETKLSTEPSP	DFSNYSEIAK	700
FEKSVPEHAE	LVEDSSPESE	PVDLFSDDSI	PEVPQTQEEA	VMLMKESLTE	
VSETVAQHKE	ERLSASPQEL	GKPYLESFQP	NLHSTKDAAS	NDIPTLTKKE	800
KISLQMEEFN	TAIYSNDDLL	SSKEDKIKES	ETFSDSSPIE	IIDEFPTFVS	
AKDDSPKLAK	EYTDLEVSDK	SEIANIQSGA	DSLPCLELPC	DLSFKNIYPK	900
DEVHVSDEFS	ENRSSVSKAS	ISPSNVSALE	PQTEMGSIVK	SKSLTKEAEK	
KLPSDTEKED	RSLSAVLSAE	LSKTSVVDLL	YWRDIKKTGV	VFGASLFLLL	1000
SLTVFSIVSV	TAYIALALLS	VTISFRIYKG	VIQAIQKSDE	GHPFRAYLES	
EVAISEELVQ	KYSNSALGHV	NSTIKELRRL	FLVDDLVDSL	KFAVLMWVFT	1100
YVGALFNGLT	LLILALISLF	SIPVIYERHQ	VQIDHYLGLA	NKSVKDAMAK	
IQAKIPGLKR	KAD	_			1163

Fig.6A



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MEDLDQSPLV	SSSDSPPRPQ	PAFKYQFVRE	PEDEEEEEE	EEEDEDEDLE	
ELEVLERKPA	AGLSAAPVPT	APAAGAPLMD	FGNDFVPPAP	RGPLPAAPPV	100
APERQPSWDP	SPVSSTVPAP	SPLSAAAVSP	SKLPEDDEPP	ARPPPPPPAS	
VSPQAEPVWT	PPAPAPAAPP	STPAAPKRRG	SSGSVDETLF	ALPAASEPVI	200
RSSAENMDLK	EQPGNTISAG	QEDFPSVLLE	TAASLPSLSP	LSAASFKEHE	
YLGNLSTVLP	TEGTLQENVS	EASKEVSEKA	KTLLIDRDLT	EFSELEYSEM	OOE
GSSFSVSPKA	ESAVIVANPR	EEIIVKNKDE	EEKLVSNNIL	HNQQELPTAL	
TKLVKEDEVV	SSEKAKDSFN	EKRVAVEAPM	REEYADFKPF	ERVWEVKDSK	400
EDSDMLAAGG	KIESNLESKV	DKKCFADSLE	QTNHEKDSES	SNDDTSFPST	
PEGIKDRPGA	YITCAPFNPA	ATESIATNIF	PLLGDPTSEN	KTDEKKIEEK	500
KAQIVTEKNT	STKTSNPFLV	AAQDSETDYV	TTDNLTKVTE	EVVANMPEGL	
TPDLVQEACE	SELNEVTGTK	IAYETKMDLV	QTSEVMQESL	YPAAQLCPSF	600
EESEATPSPV	LPDIVMEAPL	NSAVPSAGAS	VIQPSSSPLE	ASSVNYESIK	
HEPENPPPYE	EAMSVSLKKV	SGIKEEIKEP	ENINAALQET	EAPYISIACD	700
LIKETKLSAE	PAPDFSDYSE	MAKVEQPVPD	HSELVEDSSP	DSEPVDLFSD	
DSIPDVPQKQ	DETVMLVKES	LTETSFESMI	EYENKEKLSA	LPPEGGKPYL	800
ESFKLSLDNT	KDTLLPDEVS	TLSKKEKIPL	QMEELSTAVY	SNDDLFISKE	
AQIRETETFS	DSSPIEIIDE	FPTLISSKTD	SFSKLAREYT	DLEVSHKSEI	900
ANAPDGAGSL	PCTELPHDLS	LKNIQPKVEE	KISFSDDFSK	NGSATSKVLL	
LPPDVSALAT	QAEIESIVKP	KVLVKEAEKK	LPSDTEKEDR	SPSAIFSAEL	1000
SKTSVVDLLY	WRDIKKTGVV	FGASLFLLLS	LTVFSIVSVT	AYIALALLSV	
TISFRIYKGV	IQAIQKSDEG	HPFRAYLESE	VAISEELVQK	YSNSALGHVN	1100
CTIKELRRLF	LVDDLVDSLK	FAVLMWVFTY	VGALFNGLTL	LILALISLFS	
VPVIYERHQA	QIDHYLGLAN	KNVKDAMAKI	QAKIPGLKRK	AE	1192

Fig.6B

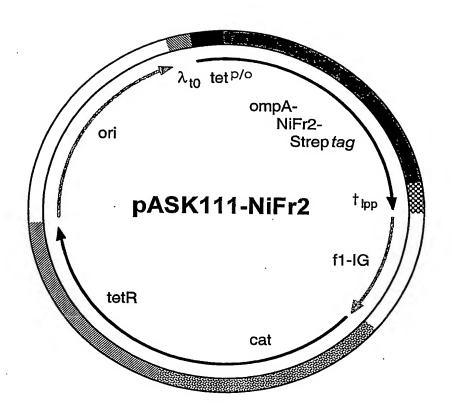


Fig. 7

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